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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Oct 11 14:24:59 EDT 2007

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Reviewer Comments:

<210> 3

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Engineered Aequorea-related fluorescent protein

<400> 3

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60

ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac

The above <223> response mentions a protein; however, this is not a protein sequence.

<210> 6

<211> 162

<212> TYPE: PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 68 to 229

<400> 6

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
1 5 10 15

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe

Please remove the "TYPE:" heading in the above <212> response. Do not show any alphabetical headings. Also, the top amino acid line is not properly aligned with its amino acid numbers.

<210> 23
<211> 37
<212> PRT
<213> Artificial sequence
<220>
<223> His-tag amino acid sequence
<400> 23

Please provide more information in the <223> response above; please give the source of the genetic material.

Application No: 10620099 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-09-20 14:58:58.525
Finished: 2007-09-20 14:59:00.108
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 583 ms
Total Warnings: 21
Total Errors: 8
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 310	Invalid sequence type in <212> in SEQID: (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (2)
E 323	Invalid/missing amino acid numbering SEQID (6)at Protein (5)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (6)
E 323	Invalid/missing amino acid numbering SEQID (6)at Protein (10)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (11)
E 323	Invalid/missing amino acid numbering SEQID (6)at Protein (15)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

Input Set:

Output Set:

Started: 2007-09-20 14:58:58.525
Finished: 2007-09-20 14:59:00.108
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 583 ms
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Total Errors: 8
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
	This error has occurred more than 20 times, will not be displayed

<110> WACHTER, Rebekka M.
REMINGTON, S. James
<120> LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
<130> 026069-151480

<140> 10620099
<141> 2003-07-14
<150> US 09/575,847
<151> 2000-05-19
<150> US 08/974,737
<151> 1997-11-19
<150> US 08/911,825
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<150> US 08/706,408
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<151> 1996-08-16
<160> 23
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<210> 1
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<212> DNA
<213> Aequorea victoria
<400> 1

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aaacttacct ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt      180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg      240
catgactttt tcaagagtgc catgcccga ggttatgtac agcaaagaac tatatttttc      300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaagggtga tacccttggt      360
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ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga      480
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tattatcaac aaaatactcc aattctcgat ggccctgtcc ttttaccaga caaccattac      600
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt      660
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<210> 2
<211> 238
<212> PRT
<213> Aequorea victoria
<400> 2

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20          25          30
Gly Glu Gly Asp Val Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35          40          45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50          55          60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Gln Arg
85          90          95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100         105         110
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Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
	115						120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145				150						155					160
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
			165					170						175	
Gln	Leu	Ala	Asp	Tyr	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Leu	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195				200						205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
225					230					235					

<210> 3

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Engineered Aequorea-related fluorescent protein

<400> 3

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ggcaagctga	ccctgaagtt	catctgcacc	accggcaagc	tgcccggtgc	ctggcccacc	180
ctcgtgacca	ccttcggcta	cggcgtgcag	tgtttcgccc	gctaccccga	ccacatgaag	240
cagcaggact	tcttcaagtc	cgccatgccc	gaaggctacg	tccaggagcg	caccatcttc	300
ttcaaggacg	acggcaacta	caagaccgcg	gccgaggtga	agttcgaggg	cgacaccctg	360
gtgaaccgca	tcgagctgaa	gggcatcgac	ttcaaggacg	acggcaacat	cctggggcac	420
aagctggagt	acaactacaa	cagccacaac	gtctatatca	tggccgacaa	gcagaagaac	480
ggcatcaagg	tgaacttcaa	gatccgccac	aacatcgagg	acggcagcgt	gcagcccgcc	540
gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgtgtgtgcc	cgacaaccac	600
tacctgagct	accagtccgc	cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	660
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<210> 4

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Engineered Aequorea-related fluorescent protein

<400> 4

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
		20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35				40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50				55				60						
Phe	Gly	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65				70					75					80	
Gln	Gln	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85				90						95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu

	100		105		110										
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	115						120					125			
Ile	Asp	Phe	Lys	Asp	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					160
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165					170					175		
Val	Gln	Pro	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu
	195					200						205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	
225					230					235					

<210> 5

<211> 63

<212> PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 2 to 64

<400> 5

Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu
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Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly
			20					25					30		
Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr
		35				40					45				
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<210> 6

<211> 162

<212> TYPE: PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 68 to 229

<400> 6

Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe
1			5						10					15	
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe
		20						25					30		
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu
		35				40						45			
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys
	50				55						60				
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser
65				70					75					80	
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val
			85					90					95		
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala
		100						105					110		

Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu
			115					120					125		
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro
		130				135					140				
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145					150					155					160
Gly	Ile														

<210> 7

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Mutant Green Fluorescent Protein

<400> 7

Cys	Phe	His	Leu	Gln	Arg	Trp	Tyr	Glx
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<210> 8

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Mutant Green Fluorescent Protein

<400> 8

Phe	Tyr	His	Cys	Leu	Arg
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<210> 9

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Mutant Green Fluorescent Protein

<400> 9

Ala	Val	Phe	Ser
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<210> 10

<211> 6

<212> PRT

<213> Artificial sequence

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<223> Mutant Green Fluorescent Protein

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Asp	Glu	His	Lys	Asn	Gln
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<210> 11

<211> 4

<212> PRT

<213> Artificial sequence

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<223> Mutant Green Fluorescent Protein

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Phe	Tyr	His	Leu
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Trp Cys Phe Leu
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<210> 13
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<223> Mutant Green Fluorescent Protein
<400> 13
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1 5

<210> 14
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Phe Tyr Asn Ile
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<210> 15
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<400> 15
Cys His Gln Arg Trp Tyr Glx
1 5

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<400> 16
Phe His Leu Gln Arg Trp Tyr Glx
1 5

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<223> Mutant Green Fluorescent Protein
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<223> Mutant Green Fluorescent Protein
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 Lys Arg Glu Gly
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<210> 19
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<223> Mutant Green Fluorescent Protein
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 His Lys Asn Pro Gln Thr
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<223> Localization sequence targeting the nucleus
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 1 5

<210> 21
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 <212> PRT
 <213> Artificial sequence
 <220>

<223> Localization sequence targeting mitochondrion
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 1 5 10 15
 Phe Arg Asn Ile Leu Arg Leu Gln Ser Thr
 20 25

<210> 22
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 <213> Artificial sequence
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<223> Localization sequence targeting the endoplasmic reticulum
 <400> 22
 Lys Asp Glu Leu
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<211> 37

<212> PRT

<213> Artificial sequence

 $\langle 220 \rangle$

<223> His-tag amino acid sequence

<400> 23

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20 25 30

Pro Pro Ala Glu Phe

35